

Please insert the following paragraph in place of the fifth full paragraph on page 4 of the specification:

B² Figure 12 (SEQ ID NOS: 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, and 102) depicts the comparison of the predicted amino acid sequences of the BVH-11 open reading frames from WU2, Rx1, JNR.7/87, SP64, P4241, A66 and SP63 S. pneumoniae strains by using the program Clustal W from MacVector sequence analysis software (version 6.5). Underneath the alignment, there is a consensus line where * and . characters indicate identical and similar amino acid residues, respectively.

Please insert the herewith enclosed substitute Sequence Listing in place of the Sequence Listing submitted on March 8, 2001 immediately following the Abstract.

REMARKS

In response to the Notice, Applicants submit a substitute Sequence Listing both in paper and computer readable form in full compliance with the Sequence Rules as set forth in 37 C.F.R. § 1.821 through 1.825. The Sequence Listing in no way introduces new matter into the specification.

In accordance with 37 C.F.R. § 1.821(f) the undersigned representative hereby states that the information recorded in computer readable form is identical to the written sequence listing. Moreover, the paper copy and above-referenced computer readable copy do not introduce new matter into the application.

Prompt and favorable consideration on the merits of the application is respectfully requested.

Date: 8/10/2001

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

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IN THE SPECIFICATION:

Figure 11 (SEQ ID NOS: 84, 85, 86, 87, 88, and 89) depicts the comparison of the predicted amino acid sequences of the BVH-3 open reading frames from WU2, RX1, JNR.7/87, SP64, P4241 and A66 S. pneumoniae strains by using the program Clustal W from MacVector sequence analysis software (version 6.5). Underneath the alignment, there is a consensus line where * and . characters indicate identical and similar amino acid residues, respectively.

Figure 12 (SEQ ID NOS: 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, and 102) depicts the comparison of the predicted amino acid sequences of the BVH-11 open reading frames from WU2, Rx1, JNR.7/87, SP64, P4241, A66 and SP63 S. pneumoniae strains by using the program Clustal W from MacVector sequence analysis software (version 6.5). Underneath the alignment, there is a consensus line where * and . characters indicate identical and similar amino acid residues, respectively.